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SEQUENCE LISTING

<110> WARE, CARL F.

<120> LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND
METHODS OF USE

<130> 051501/0276397

<140> 09/549,096

<141> 2000-04-12

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Artificial Sequence

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<213> Homo sapiens

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 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
 5 10 15

cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg 153
Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val
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gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201
Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu
40 45 50

gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249
Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
55 60 65

atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297
Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
70 75 80

ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345
Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
85 90 95

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Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu
100 105 110 115

act cag ctg ggc ctg gcc tcc ctg agg ggc ctc agc tac cac gat ggg 441
Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr His Asp Gly
120 125 130

gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489
Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
135 140 145

cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
150 155 160

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cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585
His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu
165 170 175

ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg 633
Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
180 185 190 195

gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct 681
Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
200 205 210

ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
215 220 225

cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
230 235 240

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Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
35 40 45

Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
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Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
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Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
85 90 95

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		115					120					125			
His	Asp	Gly	Ala	Leu	Val	Val	Thr	Lys	Ala	Gly	Tyr	Tyr	Tyr	Ile	Tyr
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Ser	Lys	Val	Gln	Leu	Gly	Gly	Val	Gly	Cys	Pro	Leu	Gly	Leu	Ala	Ser
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Thr	Ile	Thr	His	Gly	Leu	Tyr	Lys	Arg	Thr	Pro	Arg	Tyr	Pro	Glu	Glu
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225					230					235					240